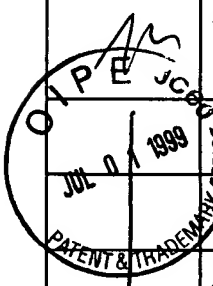
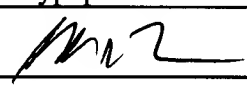
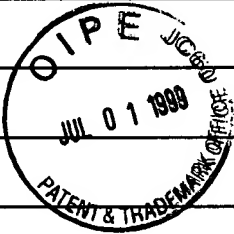


			ATTY. DOCKET NO. 06137.0021.US02	APPLICATION NO. 09/181,601
FORM PTO-1449 INFORMATION DISCLOSURE STATEMENT			APPLICANT: Stephen Anderson, <i>et al.</i>	
			FILING DATE: October 29, 1998	GROUP ART UNIT: 4643/65
OTHER (Including Author, Title, Date, Pertinent Pages, etc.)				
	AA	2 ✓	Grzesiek, <i>et al.</i> , "A simple and sensitive experiment for measurement for measurement of J _{CC} couplings between backbone carbonyl and methyl carbons in isotopically enriched proteins" <i>J. Biomol. NMR</i> 3 : 487-93 (1993).	
	AB	2 ✓	Holm, <i>et al.</i> , "Alignment of Three-Dimensional Protein Structures: Network Server for Database Searching" <i>Methods Enzymol.</i> 266 : 653-62 (1996).	
	AC	2 ✓	Holm, <i>et al.</i> , "Protein Structure Comparison by Alignment of Distance Matrices" <i>J. Mol. Biol.</i> 233 : 123-38 (1993).	
	AD	2 ✓	Holm, <i>et al.</i> , "Mapping the Protein Universe" <i>Science</i> 273 : 595-603 (1996).	
	AE	2 ✓	Holm, <i>et al.</i> , "X-ray Crystal Structure of the protease Inhibitor Domain of Alzheimer's Amyloid β -Protein Precursor" <i>Science</i> 273 : 595-603 (1996).	
	AF	2 ✓	Ikura, <i>et al.</i> , "Heteronuclear 3D NMR and Isotopic Labeling of Calmodulin" <i>Biochem. Pharmacol.</i> 40 : 153-60 (1990).	
	AG	2 ✓	Ikura, <i>et al.</i> , "An efficient NMR approach for obtaining sequence-specific resonance assignments of larger proteins based on multiple isotopic labeling" <i>FEBS Lett.</i> 266 : 155-58 (1990).	
	AH	2 ✓	Ikura, <i>et al.</i> , "Macromolecular Binding Equilibria in the <i>lac</i> Repressor System: Studies Using High-Pressure Fluorescence Spectroscopy" <i>Biochem.</i> 29 : 4659-67 (1990).	
	AI	2 ✓	Kumar, <i>et al.</i> , "Algorithms for Constraint-Satisfaction Problems: A Survey" <i>Artificial Intelligence Mag.</i> , Spring : 32-44 (1992).	
	AJ	2 ✓	Laity, <i>et al.</i> , "Structural Characterization of an Analog of the Major Rate-Determining Disulfide Folding Intermediate of Bovine Pancreatic Ribonuclease A" <i>Biochem.</i> 36 : 12683-99 (1997).	
	AK	2 ✓	Lyons, <i>et al.</i> , "An Improved Strategy for Determining Resonance Assignments for Isotopically Enriched Proteins and Its Application to an Engineered Domain of Staphylococcal Protein A" <i>Biochemistry</i> 32 : 7839-45 (1993).	
	AL	2 ✓	Madej, <i>et al.</i> , "Metal Search: A Computer Program That Helps Design Tetrahedral Metal-Binding Sites" <i>Proteins</i> 23 : 256-69 (1995).	
	AM	2 ✓	Meadows, "A computer-based protocol for semiautomated assignments and 3D structure determination of proteins" <i>J. Biomol. NMR</i> 4 : 79-86 (1994).	
	AN	2 ✓	Montelione, <i>et al.</i> , "Imaging and Localized Spectroscopy of ¹³ C by Polarization Transfer" <i>J. Magn. Res.</i> 83 : 183-88 (1990).	
	AO	2 ✓	Montelione, <i>et al.</i> , "Sequence-specific ¹ H-NMR assignments and identification of two small antiparallel β -sheets in the solution structure of recombinant human transforming growth factor α " <i>Proc. Natl. Acad. Sci (U.S.A)</i> 86 : 1519-23 (1989).	
AP	2 ✓	Montelione, <i>et al.</i> , "A General Approach for Determining Scalar Coupling Constants in Polypeptides and Proteins" <i>Biopolymers</i> 32 : 327-34 (1992).		
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			FILING DATE: October 29, 1998	GROUP ART UNIT: 1643/655
OTHER (Including Author, Title, Date, Pertinent Pages, etc.)				
<i>12</i>	AA	<u>4</u> ✓	Yamazaki, <i>et al.</i> , "Secondary structure and signal assignments of human-immunodeficiency-virus-1 protease complexed to a novel, structure-based inhibitor" <i>Eur. J. Biochem.</i> 219 : 707-12 (1994). ✓	
<i>1</i>	AB	<u>4</u> ✓	Zimmerman, <i>et al.</i> , "Automated sequencing of amino acid spin systems in proteins using multidimensional HCC(CO)NH-TOCSY spectroscopy and constraint propagation methods from artificial intelligence" <i>J. Biomol. NMR</i> 4 : 241-256 (1994). ✗	
<i>1</i>	AC	<u>4</u> ✓	Zimmerman, <i>et al.</i> , "Automated analysis of nuclear magnetic resonance assignments for proteins" <i>Curr. Opin. Struct. Bio.</i> 5 : 644-73 (1995). ✗	
<i>12</i>	AD	<u>4</u> ✓	Zimmerman, <i>et al.</i> , "Automated Analysis of Protein NMR Assignments Using Methods from Artificial Intelligence" <i>J. Mol. Bio.</i> 269 : 592-610 (1997). ✗	
	AE	<u>4</u>		
	AF	<u>4</u>		
	AG	<u>4</u>		
	AH	<u>4</u>		
	AI	<u>4</u>		
	AJ	<u>4</u>		
	AK	<u>4</u>		
	AL	<u>4</u>		
	AM	<u>4</u>		
	AN	<u>4</u>		
	AO	<u>4</u>		
	AP	<u>4</u>		
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EXAMINER <i>12</i>				
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			FILING DATE: October 29, 1998	GROSS FEE: \$1,155
OTHER (Including Author, Title, Date, Pertinent Pages, etc.)				
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	AB	1 ✓	Billeter, <i>et al.</i> , "Sequential Resonance Assignments in Protein ¹ H Nuclear Magnetic Resonance Spectra" <i>J. Mol. Biol.</i> 155 : 321-46 (1982).	
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	AD	1 ✓	Bork, <i>et al.</i> , "From genome sequences to protein function" <i>Curr. Opin. Struct. Bio.</i> 4 : 393-403 (1994).	
	AE	1 ✓	Branden, <i>et al.</i> <i>Introduction to Protein Structure</i> pp. 11-31 and 43-57 (New York: Garland Publishing, Inc., 1991).	
	AF	1 ✓	Brenner, <i>et al.</i> , "Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships" <i>Proc. Natl. Acad. Sci (U.S.A.)</i> 95 : 6073-78 (1998).	
	AG	1 ✓	Chiang, <i>et al.</i> , "Structural Studies on the Cysteine-Rich N-terminal Domain of the Alzheimer's Amyloid β Peptide Precursor Protein" <i>Neurobiol. Aging, Supplement</i> 17(4S) : abstract 393 (1996).	
	AH	1 ✓	Clore, <i>et al.</i> , "Multidimensional heteronuclear Nuclear Magnetic Resonance of Proteins" <i>Methods Enzymol.</i> 239 : 349-63 (1994).	
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	AN	1 ✓	Go, "Protein structures and split genes" <i>Advances in Biophysics</i> 19 : 91-131 (Elsevier, 1995).	
12	AO	1 ✓	Gouzey, <i>et al.</i> , "Graphical interface for ProDom domain families" <i>Trends Biochem. Sci.</i> , 21 : 493 (1994).	
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OTHER (Including Author, Title, Date, Pertinent Pages, etc.)				
	AA	3	Montelione, <i>et al.</i> , "Solution Structure of Murine Epidermal Growth Factor Determined by NMR Spectroscopy and Refined by Energy Minimization with Restraints" <i>Biochemistry</i> 31 : 236-49 (1992).	
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	AC	3	Nilges, "Calculation of Protein Structures with Ambiguous Distance Restraints. Automated Assignment of Ambiguous NOE Crosspeaks and Disulphide Connectivities" <i>J. Mol. Biol.</i> 245 : 645-60 (1995).	
	AD	3	Olsen, <i>et al.</i> , "Evaluation of an algorithm for the automated sequential assignment of protein backbone resonances: A demonstration of the connectivity tracing assignment tools (CONTRAST) software package" <i>J. Biomol. NMR</i> 4 : 385-410 (1994).	
	AE	3	Orengo, "CATH - a hierarchic classification of protein domain structures" <i>Structure</i> 5 : 1093-1108 (1997).	
	AF	3	Patthy, <i>et al.</i> , "Introns and Exons" <i>Curr. Opin. Struc. Biol.</i> 4 : 383-92 (1994).	
	AG	3	Rios, <i>et al.</i> , "Phase labeling of C-H and C-C spin-system topologies: Application in constant-time PFG-CBCA(CO)NH experiments for discriminating amino acid spin-system types" <i>J. Biomol. NMR</i> 8 : 345-350 (1996).	
	AH	3	Sandbrink, <i>et al.</i> , "Alternative Splicing Generates Functionally Related isoforms ^{6a} " <i>Ann. NY Acad. Sci.</i> 777 : 281-87 (1996).	
	AI	3	Shang, <i>et al.</i> , "Sensitivity Enhancement of Triple-Resonance Protein NMR Spectra by Proton Evolution of Multiple-Quantum Coherences using a Simultaneous ¹ H and ¹³ C Constant-Time Evolution Period" <i>J. Amer. Chem. Soc.</i> 119 : 9274-78 (1997).	
	AJ	3	Shimotakahara, <i>et al.</i> , "NMR Structural Analysis of an Analog of an Intermediate Formed in the Rate-Determining Step of One Pathway in the Oxidative Folding of Bovine Pancreatic Ribonuclease A: Automated Analysis of ¹ H, ¹³ C, and ¹⁵ N Resonance Assignments for Wild-Type and [C65S, C72S] Mutant Forms" <i>Biochem.</i> 36 : 6915-29 (1997).	
	AK	3	Swapana, <i>et al.</i> , "Application of multiple-quantum line narrowing with simultaneous ¹ H and ¹³ C constant-time scalar-coupling evolution in PFG-HACANH and PFG-HACA(CO)NH triple-resonance experiments" <i>J. Biomol. NMR</i> 9 : 105-111 (1997).	
	AL	3	Tashiro, <i>et al.</i> , "High-resolution Solution NMR Structure of the Z Domain of Staphylococcal Protein A" <i>J. Mol. Biol.</i> 272 : 573-90 (1997).	
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	AN	3	Wuthrich, "NMR - This Other Method for Protein and Nucleic Acid Structure Determination" <i>Acta Cryst. Section D.</i> 51 : 249-70 (1995).	
	AO	3	Yashikai, <i>et al.</i> , "Genomic organization of the human amyloid beta-protein precursor gene" <i>Gene</i> 87 : 257-63 (1990).	
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